BEST AVAILABLE COPY

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Ashkenazi et al.	Attorney's Docket No: 39780-2630P1C74
Serial No:	10/020,445	Group Art Unit: 1647
Filed:	October 24, 2001	Examiner: Seharaseyon, Jegatheesan

For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME**

Commissioner for Patents
P.O. Box 1450
Alexandria, Virginia 22313-1450

DECLARATION OF AUDREY GODDARD, Ph.D.,
PAUL J. GODOWSKI, Ph.D., AUSTIN GURNEY, Ph.D.,
MARGARET ROY and WILLIAM I. WOOD, Ph.D.
UNDER 37 CFR 1.131

We, Audrey Goddard, Ph.D., Paul J. Godowski, Ph.D., Austin Gurney, Ph.D., Margaret Roy and William I. Wood, Ph.D. do hereby declare and say as follows:

1. We are the inventors of the above-identified application.

2. We have read and understood the claims pending in this application, and are aware that the claims have been rejected as anticipated by Kedra *et al.*, "Homo Sapiens mRNA for Synaptogyrin 2," Accession No. AJ002308, published on March 3, 1998.

3. We conceived and reduced to practice the polypeptide designated as PRO615 (SEQ ID NO:162) encoded by the nucleic acid sequences claimed in the above-identified application in the United States prior to March 3, 1998.

4. At the time the PRO615 polypeptide was cloned and sequenced, one of the inventors, Austin Gurney, was responsible for overseeing the cloning of cDNAs which encoded novel polypeptides, including the cDNA claimed in the above-identified application that encoded the PRO615 polypeptide (SEQ ID NO: 162).

5. At the time the PRO615 polypeptide was cloned and sequenced, one of the inventors, Audrey Goddard, was, as still is, responsible for overseeing the sequencing of novel

polypeptides, including the PRO615 polypeptide (SEQ ID NO:162) encoded by the nucleic acid sequences claimed in the above-identified application.

6. At the time the PRO615 polypeptide was cloned and sequenced, one of the inventors, William I. Wood, was, as still is, responsible for overseeing the homology searches for the novel polypeptides, including that for the PRO615 polypeptide (SEQ ID NO:162) encoded by the cDNA claimed in the above-identified application.

7. A cDNA clone, referred to as DNA48304-1323 in the above-identified application, was identified as encoding the PRO615 polypeptide.

8. The full length of the cDNA clone is shown in Figure 60 of the above-identified application. The full-length cDNA sequence has 1512 nucleotide residues. The full length of the PRO615 peptide encoded by DNA46804-1323 is shown in Figure 61 of the above-identified application. The full-length PRO615 polypeptide has 224 amino acid residues, and is homologous to human synaptogyrin.

9. Copies of the pages from the GSeqEdit database which report the cloning, sequencing and functional data for the PRO615 polypeptide sequence, including its homology to human synaptogyrin, as well as the cloning, sequencing data for the nucleic acid sequence encoding PRO615 are attached to this declaration (with the dates redacted) as Exhibit A.

10. The GSeqEdit report shows the full-length nucleic acid sequence for DNA48304-1323 (identified as "DNA48304") and the full-length PRO615 polypeptide encoded by DNA48304. Both the DNA48304 and the PRO615 polypeptide sequences and the homology of PRO615 to human synaptogyrin were obtained prior to March 3, 1998.

11. The DNA48304 sequence shown in the GSeqEdit report is identical to that of SEQ ID NO:161 disclosed in the above-identified application.

12. The beginning of the cDNA sequence corresponding to SEQ ID NO:161 in the above-identified application is shown on page 1 of the GSeqEdit database report and the location of the first nucleotide is marked with "^insert starts here" and an arrow. The

location of the last nucleotide corresponding to SEQ ID NO:161 is shown on page 11 and is marked with an arrow.

13. The amino acid sequence shown in the GSeqEdit report is identical to that of SEQ ID NO:162 disclosed in the above-identified application.

14. The amino acid residues of the PRO615 polypeptide (SEQ ID NO:162) encoded by the cDNA (DNA48304) are shown in the GSeqEdit report starting on page 2 and continuing until page 7 of the report.

15. Exhibit A clearly shows that both the full-length DNA48304 sequence and the full-length PRO615 polypeptide sequence disclosed in the above-identified application, as well as the homology of PRO615 to human synaptogyrin were obtained prior to March 3, 1998.

16. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

A. Goddard — 9/10/04

Audrey Goddard — Date

Paul J. Godowski, Ph.D. — Date

Austin Gurney, Ph.D. — Date

Margaret Roy, Ph.D. — Date

William I. Wood, Ph.D. — Date

location of the last nucleotide corresponding to SEQ ID NO:161 is shown on page 11 and is marked with an arrow.

13. The amino acid sequence shown in the GSeqEdit report is identical to that of SEQ ID NO:162 disclosed in the above-identified application.

14. The amino acid residues of the PRO615 polypeptide (SEQ ID NO:162) encoded by the cDNA (DNA48304) are shown in the GSeqEdit report starting on page 2 and continuing until page 7 of the report.

15. Exhibit A clearly shows that both the full-length DNA48304 sequence and the full-length PRO615 polypeptide sequence disclosed in the above-identified application, as well as the homology of PRO615 to human synaptogyrin were obtained prior to March 3, 1998.

16. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Audrey Goddard	Date
Paul J. Godowski, Ph.D.	9/09/2001 Date
Austin Gurney, Ph.D.	Date
Margaret Roy, Ph.D.	Date
William I. Wood, Ph.D.	Date

location of the last nucleotide corresponding to SEQ ID NO:161 is shown on page 11 and is marked with an arrow.

13. The amino acid sequence shown in the GSeqEdit report is identical to that of SEQ ID NO:162 disclosed in the above-identified application.

14. The amino acid residues of the PRO615 polypeptide (SEQ ID NO:162) encoded by the cDNA (DNA48304) are shown in the GSeqEdit report starting on page 2 and continuing until page 7 of the report.

15. Exhibit A clearly shows that both the full-length DNA48304 sequence and the full-length PRO615 polypeptide sequence disclosed in the above-identified application, as well as the homology of PRO615 to human synaptogyrin were obtained prior to March 3, 1998.

16. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Audrey Goddard	Date
Paul J. Godowski, Ph.D.	Date
Austin Gurney, Ph.D.	Date 9/7/04
Margaret Roy, Ph.D.	Date
William I. Wood, Ph.D.	Date

location of the last nucleotide corresponding to SEQ ID NO:161 is shown on page 11 and is marked with an arrow.

13. The amino acid sequence shown in the GSeqEdit report is identical to that of SEQ ID NO:162 disclosed in the above-identified application.

14. The amino acid residues of the PRO615 polypeptide (SEQ ID NO:162) encoded by the cDNA (DNA48304) are shown in the GSeqEdit report starting on page 2 and continuing until page 7 of the report.

15. Exhibit A clearly shows that both the full-length DNA48304 sequence and the full-length PRO615 polypeptide sequence disclosed in the above-identified application, as well as the homology of PRO615 to human synaptogyrin were obtained prior to March 3, 1998.

16. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Audrey Goddard	Date
Paul J. Godowski, Ph.D.	Date
Austin Gurney, Ph.D.	Date
Margaret Roy, [redacted]	Date 9/16/04
William I. Wood, Ph.D.	Date

SV 2060995 v1
9/7/04 3:34 PM (39780.2630)

location of the last nucleotide corresponding to SEQ ID NO:161 is shown on page 11 and is marked with an arrow.

13. The amino acid sequence shown in the GSeqEdit report is identical to that of SEQ ID NO:162 disclosed in the above-identified application.

14. The amino acid residues of the PRO615 polypeptide (SEQ ID NO:162) encoded by the cDNA (DNA48304) are shown in the GSeqEdit report starting on page 2 and continuing until page 7 of the report.

15. Exhibit A clearly shows that both the full-length DNA48304 sequence and the full-length PRO615 polypeptide sequence disclosed in the above-identified application, as well as the homology of PRO615 to human synaptogyrin were obtained prior to March 3, 1998.

16. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Audrey Goddard	Date
Paul J. Godowski, Ph.D.	Date
Austin Gurney, Ph.D.	Date
Margaret Roy, Ph.D.	Date
William I. Wood, Ph.D.	9/9/04 Date

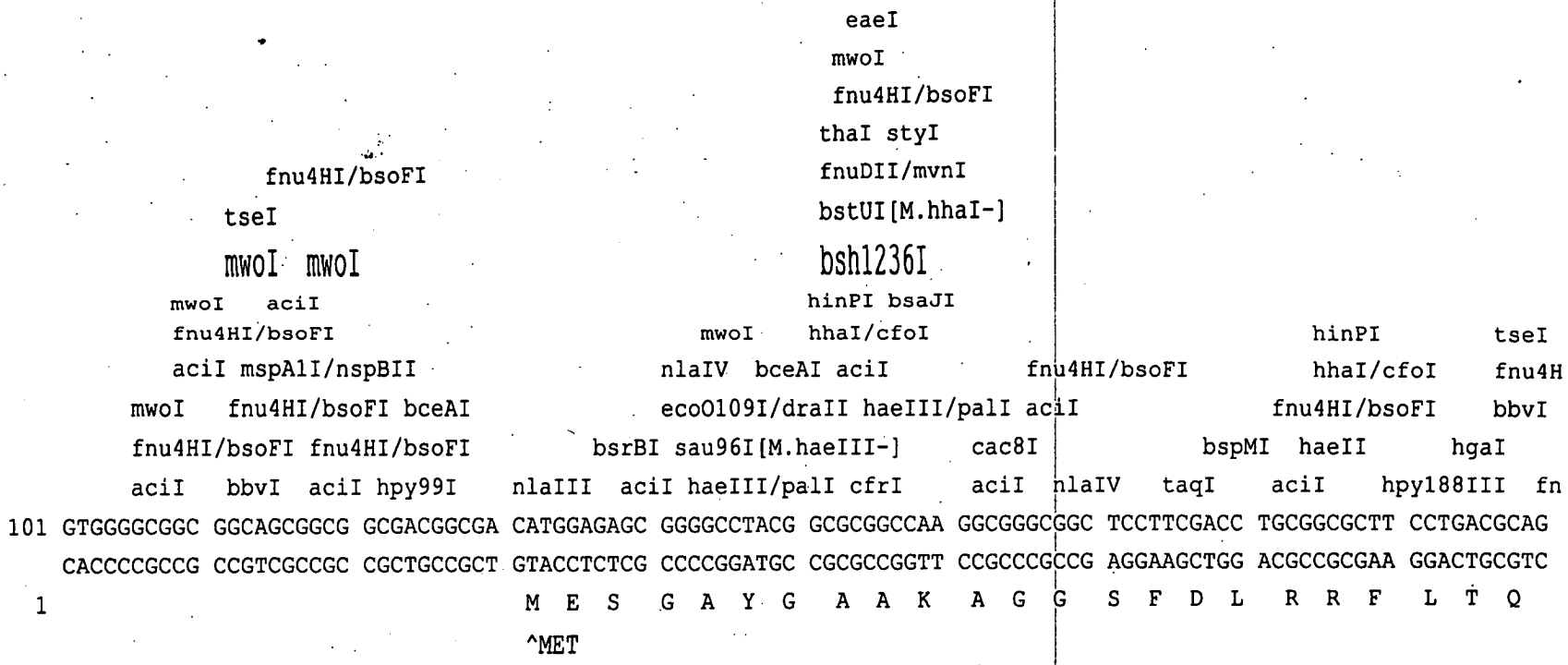
>[redacted]

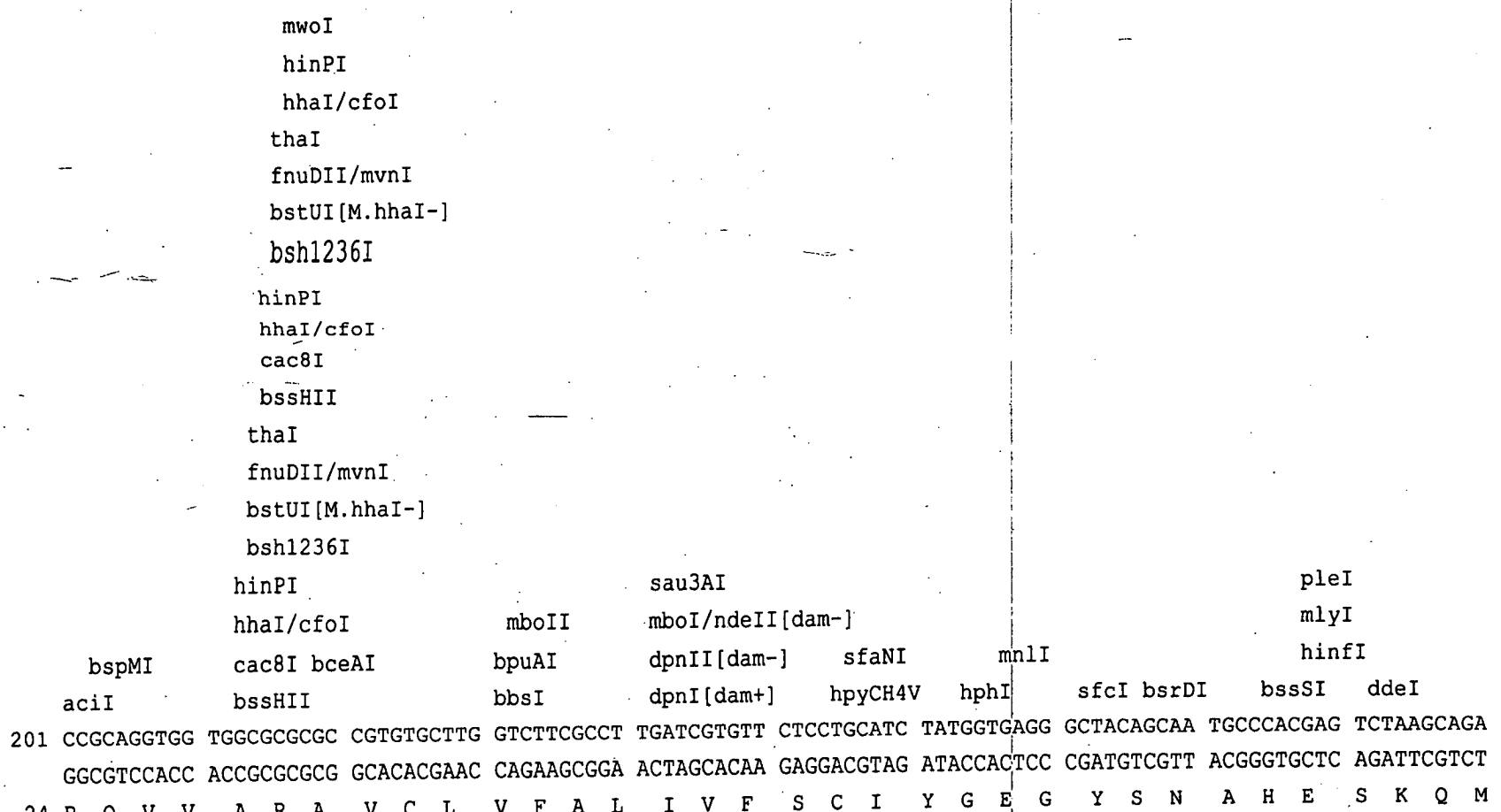
>DNA48304 [Full]

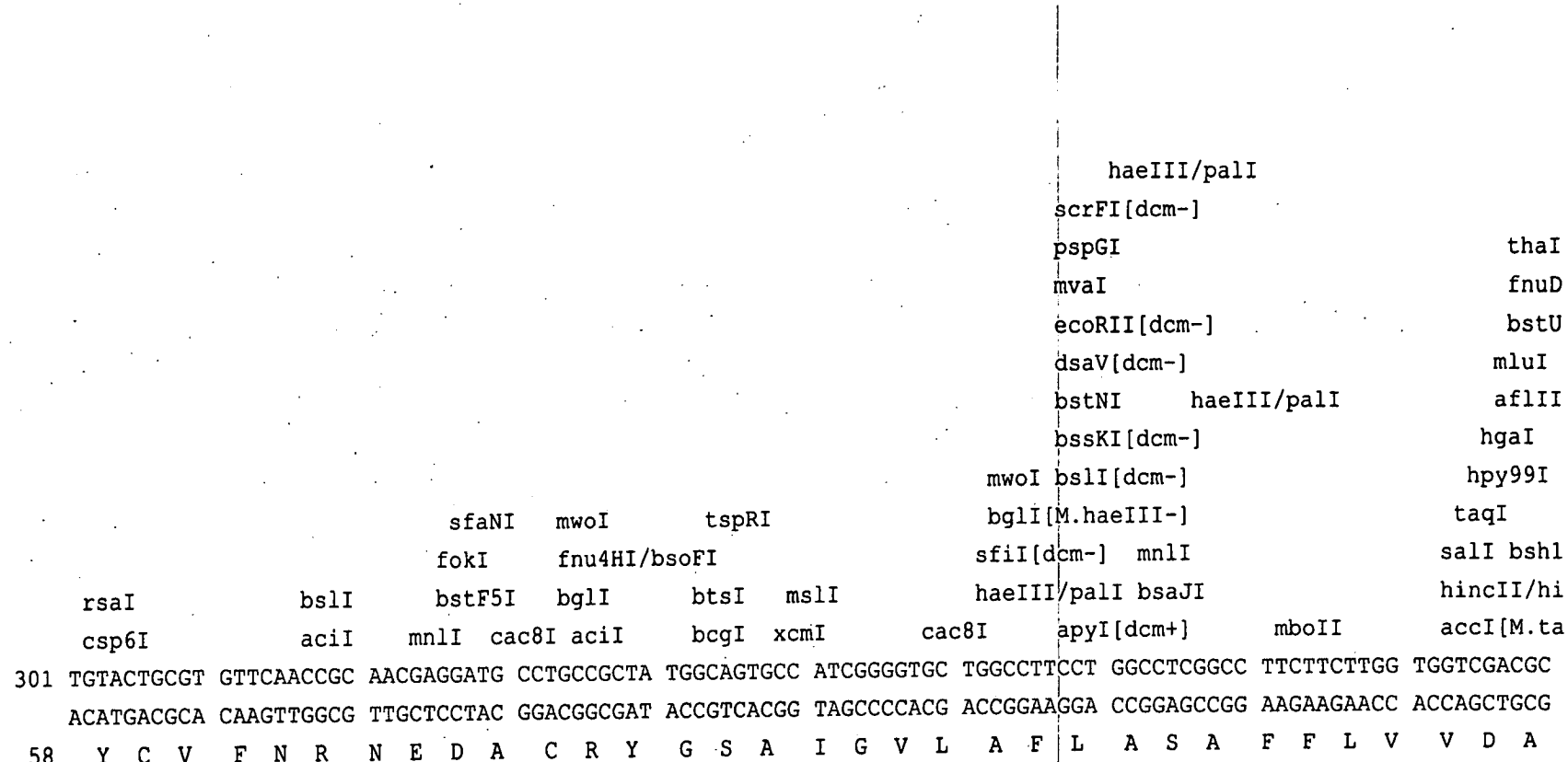
>707 Sites [All Sites]

>[redacted]DNA48304 brush GSeqEdit

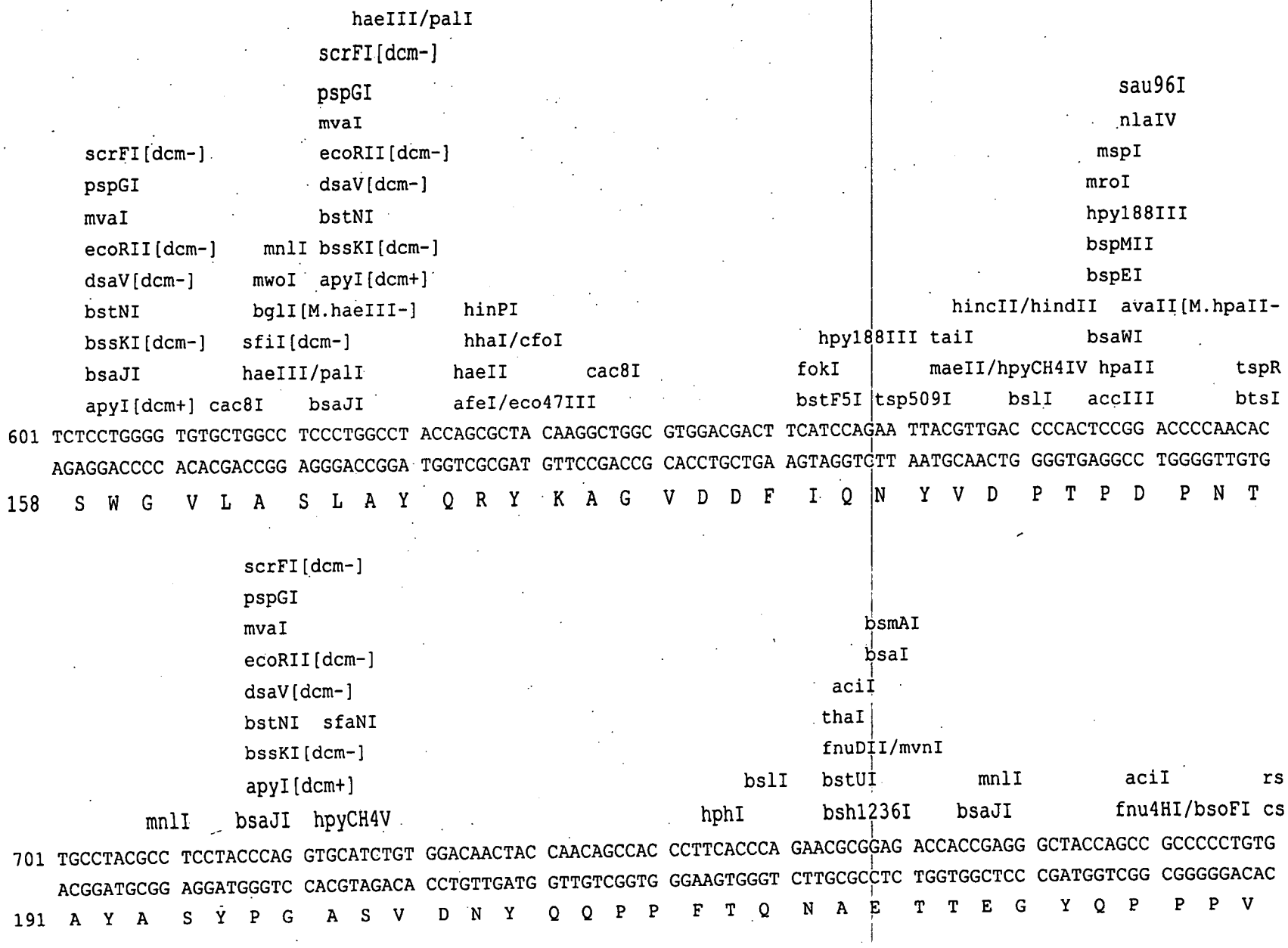
```
                                                
```


eaeI
mwoI
fnu4HI/bsoFI
thaI styI
fnuDII/mvnI
bstUI[M.hhaI-]
bsh1236I
hinPI bsaJI
fnu4HI/bsoFI
tseI
mwoI mwoI
mwoI aciI
fnu4HI/bsoFI
mwoI hhaI/cfoI
hinPI tseI
aciI mspA1I/nspBII
nlaIV bceAI aciI
fnu4HI/bsoFI
hhaI/cfoI fnu4H
mwoI fnu4HI/bsoFI bceAI
eco0109I/draII haeIII/palI aciI
fnu4HI/bsoFI bbvI
fnu4HI/bsoFI fnu4HI/bsoFI
bsrBI sau96I[M.haeIII-]
cac8I
bspMI haeII hgaI
aciI bbvI aciI hpy99I
nlaIII aciI haeIII/palI cfrI
aciI nlaIV taqI aciI hpy188III fn
101 GTGGGGCGGC GGCAGCGGCG GCGACGGCGA CATGGAGAGC GGGGCCTACG GCGCGGCCAA GGCGGGCGGC TCCTTCGACC TGCGGCGCTT CCTGACGCAG
CACCCCGCCG CCGTCGCCGC CGCTGCCGCT GTACCTCTCG CCCCGGATGC CGCGCCGGTT CCGCCCGCCG AGGAAGCTGG ACGCCGCGAA GGACTGCGTC
1 M E S G A Y G A A K A G G S F D L R R F L T Q
^MET


mwoI
hinPI
hhaI/cfoI
thaI
fnuDII/mvnI
bstUI[M.hhaI-]
bsh1236I
hinPI
hhaI/cfoI
cac8I
bssHII
thaI
fnuDII/mvnI
bstUI[M.hhaI-]
bsh1236I
hinPI
hhaI/cfoI
sau3AI
mboII
mboI/ndeII[dam-]
pleI
mlyI
hinfI
bspMI
cac8I bceAI
bpuAI
dpnII[dam-]
sfaNI
mnlI
aciI
bssHII
bbsI
dpnI[dam+]
hpyCH4V
hphI
sfcI bsrDI
bssSI
ddeI
201 CCGCAGGTGG TGGCGCGCGC CGTGTGCTTG GTCTTCGCCT TGATCGTGTT CTCCTGCATC TATGGTGAGG GCTACAGCAA TGCCCACGAG TCTAAGCAGA
GGCGTCCACC ACCGCGCGCG GCACACGAAC CAGAAGCGGA ACTAGCACAA GAGGACGTAG ATACCACTCC CGATGTCGTT ACGGGTGCTC AGATTCGTCT
24 P Q V V A R A V C L V F A L I V F S C I Y G E G Y S N A H E S K Q M


haeIII/palI
scrFI[dcm-]
pspGI
thaI
mvaI
fnuD
ecoRII[dcm-]
bstU
dsaV[dcm-]
mluI
bstNI
haeIII/palI
aflII
bssKI[dcm-]
hgaI
mwoI
bslI[dcm-]
hpy99I
sfaNI
mwoI
tspRI
bglI[M.haeIII-]
taqI
fokI
fnu4HI/bsoFI
sfiI[dcm-]
mnlI
salI bsh1
rsaI
bslI
bstF5I
bglI
btsI
mslI
haeIII/palI
bsaJI
hincII/hi
csp6I
aciI
mnlI
cac8I
aciI
bcgI
xcmI
cac8I
apyI[dcm+]
mboII
accI[M.ta
301 TGTACTGCGT GTTCAACCGC AACGAGGATG CCTGCCGCTA TGGCAGTGCC ATCGGGGTGC TGGCCTTCCT GGCCTCGGCC TTCTTCTTGG TGGTCGACGC
ACATGACGCA CAAGTTGGCG TTGCTCCTAC GGACGGCGAT ACCGTCACGG TAGCCCCACG ACCGGAAGGA CCGGAGCCGG AAGAAGAACC ACCAGCTGCG
58 Y C V F N R N E D A C R Y G S A I G V L A F L A S A F F L V V D A

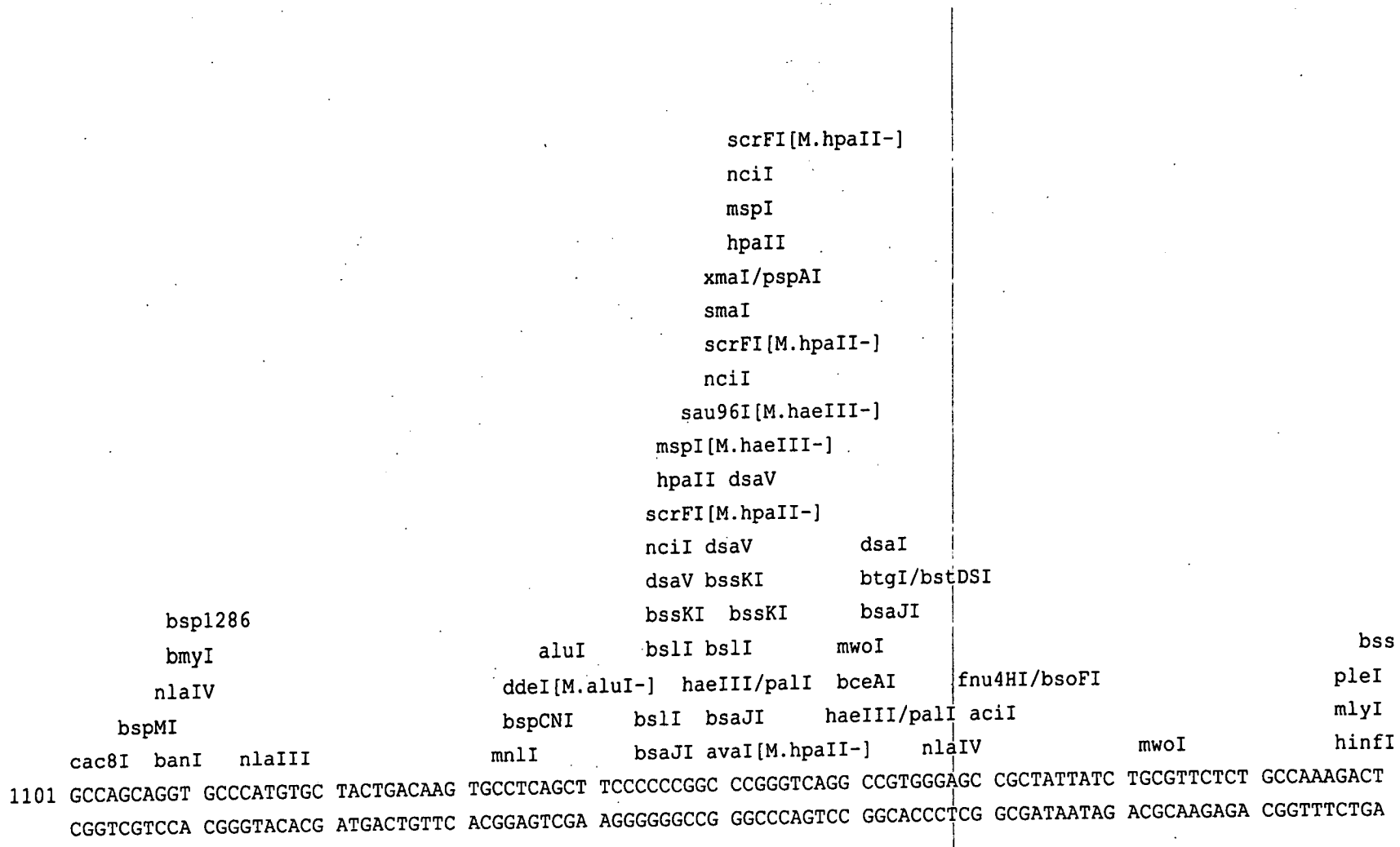
```
                                                scrFI[dcm-]
                                                pspGI
                                                mvaI
                                                ecoRII[dcm-]
                                                dsaV[dcm-]
                                                bstNI
                                                bssKI[dcm-]
                sau3AI                          apyI[dcm+]   tsp45I        ddeI[M.aluI-]  bslI
                mboI/ndeII[dam-]               sexAI         maeIII  earI/ksp632I       sau96I
                dpnII[dam-]                 rsaI          hphI bspMI mboII   aluI      avaII
                dpnI[dam+]   tspRI  aciI  csp6I          bstEII   sapI   bspCNI   hpy188III
401 GTATTTCCCC CAGATCAGCA ACGCCACTGA CCGCAAGTAC CTGGTCATTG GTGACCTGCT CTTCTCAGCT CTCTGGACCT TCCTGTGGTT TGTTGGTTTC
    CATAAAGGGG GTCTAGTCGT TGCGGTGACT GGCGTTCATG GACCAGTAAC CACTGGACGA GAAGAGTCGA GAGACCTGGA AGGACACCAA ACAACCAAAG
 91  Y   F   P   Q   I   S   N   A   T   D   R   K   Y   L   V   I   G   D   L   L   F   S   A   L   W   T   F   L   W   F   V   G   F

                                                                  pleI
                                                               haeIII/palI      tseI
                pflMI           hphI            taiI          sau96I[M.haeIII-] fnu4HI/bsoFI
             hphI    bsrI       tsp45I          maeII/hpyCH4IV    mlyI          bbvI            aluI
          mnlI  bslI tspRI     maeIII     bcgI btrI          nlaIV hinfI    mnlI        hphI eco57I            mboI
501 TGCTTCCTCA CCAACCAGTG GGCAGTCACC AACCCGAAGG ACGTGCTGGT GGGGGCCGAC TCTGTGAGGG CAGCCATCAC CTTCAGCTTC TTTTCCATCT
    ACGAAGGAGT GGTTGGTCAC CCGTCAGTGG TTGGGCTTCC TGCACGACCA CCCCCGGCTG AGACACTCCC GTCGGTAGTG GAAGTCGAAG AAAAGGTAGA
124  C   F   L   T   N   Q   W   A   V   T   N   P   K   D   V   L   V   G   A   D   S   V   R   A   A   I   T   F   S   F   F   S   I   F
```

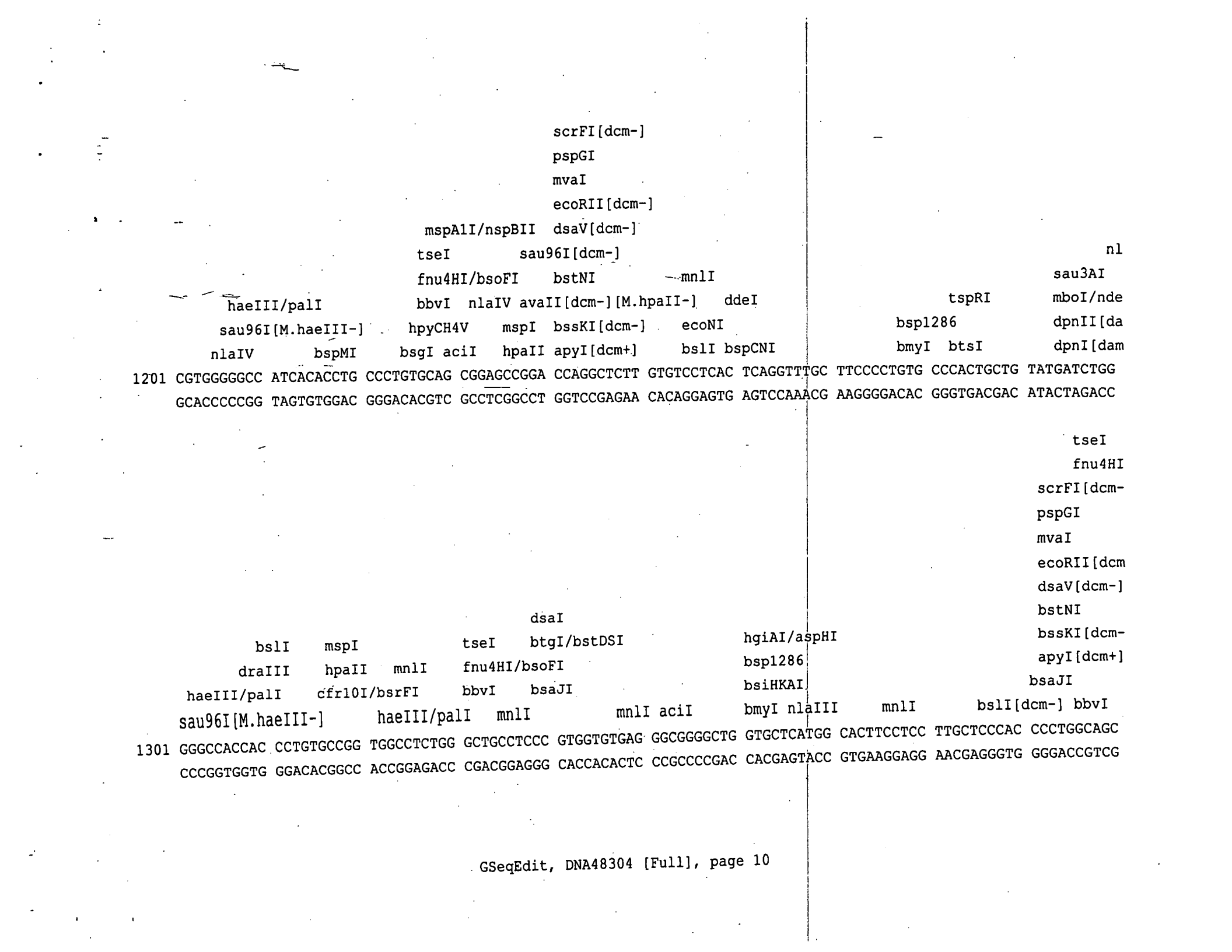

haeIII/palI
scrFI[dcm-]
pspGI
mvaI
ecoRII[dcm-]
dsaV[dcm-]
bstNI
bssKI[dcm-]
mnlI
mwoI
apyI[dcm+]
bglI[M.haeIII-]
sfiI[dcm-]
haeIII/palI
cac8I
bsaJI
hinPI
hhaI/cfoI
haeII
afeI/eco47III
cac8I
sau96I
nlaIV
mspI
mroI
hpy188III
bspMII
bspEI
hincII/hindII
avaII[M.hpaII-
bsaWI
hpy188III
taiI
fokI
maeII/hpyCH4IV
hpaII
tspR
bstF5I
tsp509I
bslI
accIII
btsI
601 TCTCCTGGGG TGTGCTGGCC TCCCTGGCCT ACCAGCGCTA CAAGGCTGGC GTGGACGACT TCATCCAGAA TTACGTTGAC CCCACTCCGG ACCCCAACAC
AGAGGACCCC ACACGACCGG AGGGACCGGA TGGTCGCGAT GTTCCGACCG CACCTGCTGA AGTAGGTCTT AATGCAACTG GGGTGAGGCC TGGGGTTGTG
158 S W G V L A S L A Y Q R Y K A G V D D F I Q N Y V D P T P D P N T
scrFI[dcm-]
pspGI
mvaI
ecoRII[dcm-]
dsaV[dcm-]
bstNI
sfaNI
bssKI[dcm-]
apyI[dcm+]
mnlI
bsaJI
hpyCH4V
bsmAI
bsaI
aciI
thaI
fnuDII/mvnI
bslI
bstUI
mnlI
aciI
rs
hphI
bsh1236I
bsaJI
fnu4HI/bsoFI
cs
701 TGCCTACGCC TCCTACCCAG GTGCATCTGT GGACAACTAC CAACAGCCAC CCTTCACCCA GAACGCGGAG ACCACCGAGG GCTACCAGCC GCCCCCTGTG
ACGGATGCGG AGGATGGGTC CACGTAGACA CCTGTTGATG GTTGTCGGTG GGAAGTGGGT CTTGCGCCTC TGGTGGCTCC CGATGGTCGG CGGGGGACAC
191 A Y A S Y P G A S V D N Y Q Q P P F T Q N A E T T E G Y Q P P P V

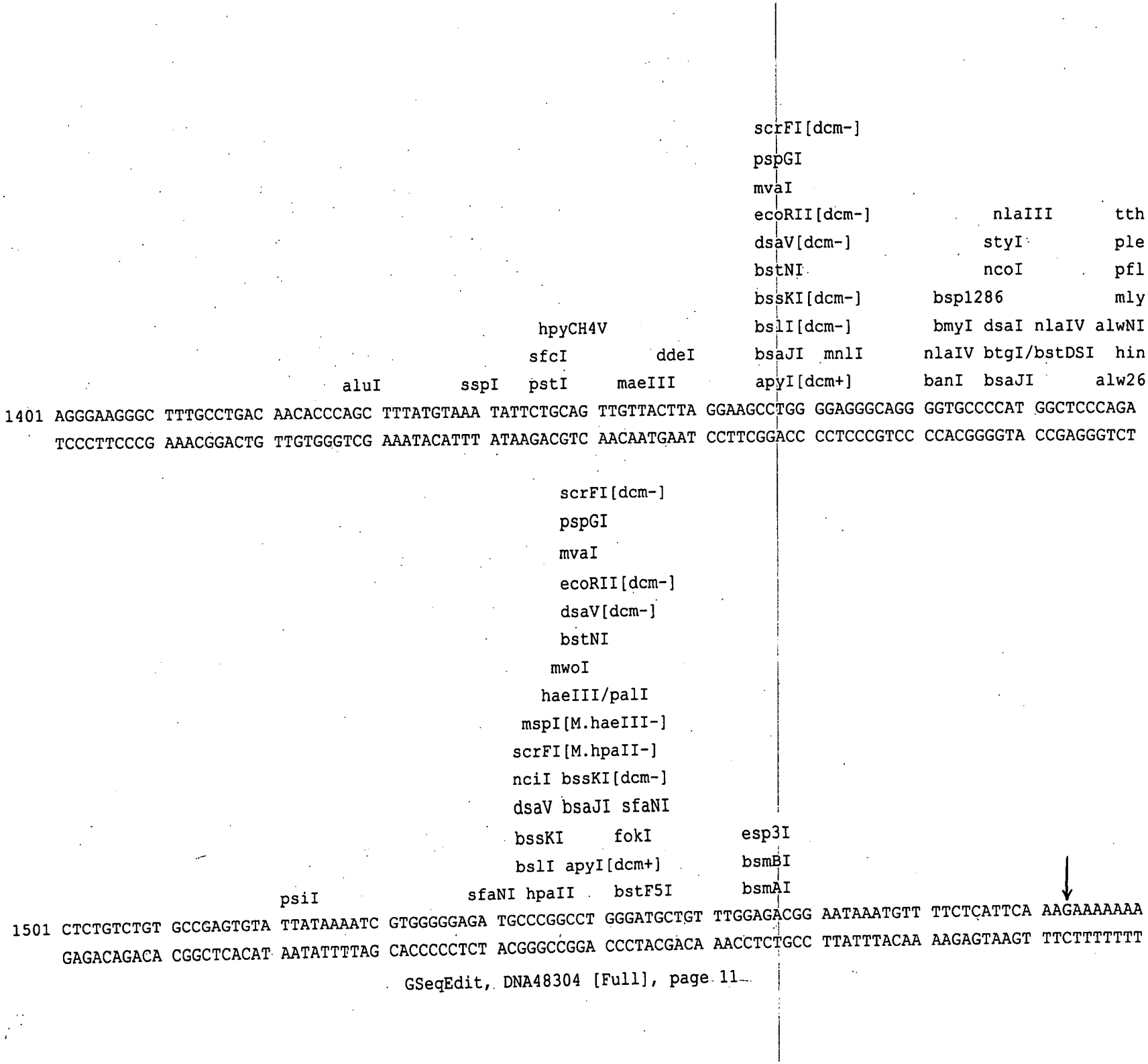
```
                                        sau96I[M.haeIII-]
                                        haeIII/palI
                                        sau96I[M.haeIII-] scrFI[dcm-]
                                        pspOMI/bsp120I    pspGI              scrFI[dcm-]
                                        nlaIV             mvaI               pspGI
                                        eco0109I/draII    ecoRII[dcm-]       mvaI
                                        bsp1286[M.haeIII-]                   ecoRII[dcm-]
                                        bmyI              dsaV[dcm-]         dsaV[dcm-]
                                        banII[M.haeIII-]  bstNI              bstNI
                                        apaI              bssKI[dcm-]        bssKI[dcm-]
    ddeI                                eco0109I/draII    apyI[dcm+]         apyI[dcm+]
    bspCNI aciI              bsmFI   mnlI   mnlI mnlI   bsaJI       xcmI   mnlI        cac8I   mnlI    hph
801 TACTGAGTGG CGGTTAGCGT GGGAAGGGGG ACAGAGAGGG CCCTCCCCTC TGCCCTGGAC TTTCCCATCA GCCTCCTGGA ACTGCCAGCC CCTCTCTTTC
    ATGACTCACC GCCAATCGCA CCCTTCCCCC TGTCTCTCCC GGGAGGGGAG ACGGGACCTG AAAGGGTAGT CGGAGGACCT TGACGGTCGG GGAGAGAAAG
224 Y  O

                                                scrFI[dcm-]
                  aluI                          pspGI
                  pvuII[M.Hl-]                  mvaI aciI
                  mspAlI/nspBII                 ecoRII[dcm-]
                 tseI                           dsaV[dcm-]
                 fnu4HI/bsoFI                   bstNI                    mwoI
                 bbvI                  mnlI     bssKI[dcm-]              bglI
          fokI   hpyCH4V          ddeI[M.aluI-]  bslI[dcm-] mwoI         bsp1286
          bstF5I bsgI          aluI   nlaIV      apyI[dcm+] cac8I         bmyI    mnlI eco57
901 ACCTGTTCCA TCCTGTGCAG CTGACACACA GCTAAGGAGC CTCATAGCCT GGCGGGGGCT GGCAGAGCCA CACCCCAAGT GCCTGTGCCC AGAGGGCTTC
    TGGACAAGGT AGGACACGTC GACTGTGTGT CGATTCCTCG GAGTATCGGA CCGCCCCCGA CCGTCTCGGT GTGGGGTTCA CGGACACGGG TCTCCCGAAG
```

scrFI[dcm-]
pspGI
mvaI
ecoRII[dcm-]
dsaV[dcm-]
bstNI
bssKI[dcm-]
tspRI
bsaJI
btsI
bpmI/gsuI[dcm-]
rmaI
sfcI
bsrBI mnlI bsp1286
maeI
ddeI pstI rmaI
aciI bseRI bmyI
bfaI
tru9I bspCNI aciI hpyCH4V maeI
fnu4HI/bsoFI apyI[dcm+]
aluI
mnlI mseI mnlI mwoI cac8I bfaI

1001 AGTCAGCCGC TCACTCCTCC AGGGCACTTT TAGGAAAGGG TTTTTAGCTA GTGTTTTTCC TCGCTTTTAA TGACCTCAGC CCCGCCTGCA GTGGCTAGAA
TCAGTCGGCG AGTGAGGAGG TCCCGTGAAA ATCCTTTCCC AAAAATCGAT CACAAAAAGG AGCGAAAATT ACTGGAGTCG GGGCGGACGT CACCGATCTT


scrFI[M.hpaII-]
nciI
mspI
hpaII
xmaI/pspAI
smaI
scrFI[M.hpaII-]
nciI
sau96I[M.haeIII-]
mspI[M.haeIII-]
hpaII dsaV
scrFI[M.hpaII-]
nciI dsaV dsaI
dsaV bssKI btgI/bstDSI
bssKI bssKI bsaJI
bsp1286
bmyI
nlaIV
bspMI
cac8I banI nlaIII
aluI
bslI bslI mwoI
ddeI[M.aluI-] haeIII/palI bceAI
bspCNI bslI bsaJI haeIII/palI aciI
mnlI bsaJI avaI[M.hpaII-] nlaIV
fnu4HI/bsoFI
mwoI
bss
pleI
mlyI
hinfI
1101 GCCAGCAGGT GCCCATGTGC TACTGACAAG TGCCTCAGCT TCCCCCCGGC CCGGGTCAGG CCGTGGGAGC CGCTATTATC TGCGTTCTCT GCCAAAGACT
CGGTCGTCCA CGGGTACACG ATGACTGTTC ACGGAGTCGA AGGGGGGCCG GGCCCAGTCC GGCACCCTCG GCGATAATAG ACGCAAGAGA CGGTTTCTGA


scrFI[dcm-]
pspGI
mvaI
ecoRII[dcm-]
mspA1I/nspBII dsaV[dcm-]
tseI sau96I[dcm-]
fnu4HI/bsoFI bstNI mnlI
haeIII/palI bbvI nlaIV avaII[dcm-][M.hpaII-] ddeI
sau96I[M.haeIII-] hpyCH4V mspI bssKI[dcm-] ecoNI
nlaIV bspMI bsgI aciI hpaII apyI[dcm+] bslI bspCNI
1201 CGTGGGGGCC ATCACACCTG CCCTGTGCAG CGGAGCCGGA CCAGGCTCTT GTGTCCTCAC TCAGGTTTGC TTCCCCTGTG CCCACTGCTG TATGATCTGG
GCACCCCCGG TAGTGTGGAC GGGACACGTC GCCTCGGCCT GGTCCGAGAA CACAGGAGTG AGTCCAAACG AAGGGGACAC GGGTGACGAC ATACTAGACC
nl
sau3AI
tspRI mboI/nde
bsp1286 dpnII[da
bmyI btsI dpnI[dam
tseI
fnu4HI
scrFI[dcm-
pspGI
mvaI
ecoRII[dcm
dsaV[dcm-]
bstNI
bssKI[dcm-
apyI[dcm+]
bsaJI
dsaI
bslI mspI tseI btgI/bstDSI hgiAI/aspHI
draIII hpaII mnlI fnu4HI/bsoFI bsp1286
haeIII/palI cfr10I/bsrFI bbvI bsaJI bsiHKAI
sau96I[M.haeIII-] haeIII/palI mnlI mnlI aciI bmyI nlaIII mnlI bslI[dcm-] bbvI
1301 GGGCCACCAC CCTGTGCCGG TGGCCTCTGG GCTGCCTCCC GTGGTGTGAG GGCGGGGCTG GTGCTCATGG CACTTCCTCC TTGCTCCCAC CCCTGGCAGC
CCCGGTGGTG GGACACGGCC ACCGGAGACC CGACGGAGGG CACCACACTC CCGCCCCGAC CACGAGTACC GTGAAGGAGG AACGAGGGTG GGGACCGTCG


scrFI[dcm-]
pspGI
mvaI
ecoRII[dcm-]
dsaV[dcm-]
bstNI
bssKI[dcm-]
bslI[dcm-]
bsaJI
apyI[dcm+]
nlaIII
styI
ncoI
bsp1286
bmyI
nlaIV
banI
tth
ple
pfl
mly
dsaI
alwNI
btgI/bstDSI
hin
bsaJI
alw26
hpyCH4V
sfcI
ddeI
mnlI
aluI
sspI
pstI
maeIII
1401 AGGGAAGGGC TTTGCCTGAC AACACCCAGC TTTATGTAAA TATTCTGCAG TTGTTACTTA GGAAGCCTGG GGAGGGCAGG GGTGCCCCAT GGCTCCCAGA
TCCCTTCCCG AAACGGACTG TTGTGGGTCG AAATACATTT ATAAGACGTC AACAATGAAT CCTTCGGACC CCTCCCGTCC CCACGGGGTA CCGAGGGTCT
scrFI[dcm-]
pspGI
mvaI
ecoRII[dcm-]
dsaV[dcm-]
bstNI
mwoI
haeIII/palI
mspI[M.haeIII-]
scrFI[M.hpaII-]
nciI bssKI[dcm-]
dsaV bsaJI sfaNI
bssKI
fokI
esp3I
bslI apyI[dcm+]
bsmBI
bsmAI
psiI
sfaNI hpaII
bstF5I
1501 CTCTGTCTGT GCCGAGTGTA TTATAAAATC GTGGGGGAGA TGCCCGGCCT GGGATGCTGT TTGGAGACGG AATAAATGTT TTCTCATTCA AAGAAAAAAA
GAGACAGACA CGGCTCACAT AATATTTTAG CACCCCCTCT ACGGGCCGGA CCCTACGACA AACCTCTGCC TTATTTACAA AAGAGTAAGT TTCTTTTTTT

thaI
fnu4HI/bsoFI
haeIII/palI
mcrI rmaI
eagI/xmaIII/eclXI
eaeI maeI
cfrI pleI
bsiEI mlyI taqI
notI fnuDII/mvnI salI
fnu4HI/bsoFI bfaI hincII/hindII[M.taqI-]
aciI bstUI xbaI accI[M.taqI-]
thaI aciI hinfI pleI
fnuDII/mvnI hpy188III
bstUI bsh1236I mlyI
bsh1236I drdI hinfI[M.taqI-]

1601 AAAAAAAAAA AAACGCGGCC GCGACTCTAG AGTCGACCTG
TTTTTTTTTT TTTGCGCCGG CGCTGAGATC TCAGCTGGAC
^pRK follows

> length: 1640

accI(GTMKAC): 393 1632
accIII(TCCGGA): 686
aciI(CCGC): 79 81 93 106 109 115 118 139 153 162 166 182 201 317 335 431 765 789
810 952 1007 1082 1170 1230 1352 1615 1619

afeI(AGCGCT): 634
aflIII(ACRYGT): 73 85 97 397
aluI(AGCT): 467 585 919 930 1046 1137 1428

alw26I(CAGNNNCTG): 1497
alwI(GGATCNNNN): 42 43 54
alwNI(CAGNNNCTG): 1497
apaI(GGGCCC): 838
apoI(RAATTY): 23
apyI(CCWGG): 368 440 604 623 717 854 875 948 1019 1241 1392 1466 1548
aspHI(GWGCWC): 1361
aspI(GACNNNGTC): 1499
avaI(CYCGRG): 1150
avaII(GGWCC): 475 689 1238
bamHI(GGATCC): 42
banI(GGYRCC): 1108 1481
banII(GRGCYC): 838
bbsI(GAAGACNNNNNN): 231
bbvI(GCAGC): 112 197 570 917 1227 1331 1396
bceAI(ACGGCNNNNNNNNNNNN): 124 148 219 1160
bcgI(NNNNNNNNNNNNCGANNNNNNTGCNNNNNNNNNNNN): 343 535
bfaI(CTAG): 49 1048 1095 1627
bglI(GCCNNNNNGGC): 30 334 363 618 987
bmyI(GDGCHC): 838 985 1022 1109 1278 1361 1482
bpmI(CTGGAG): 1017
bpuAI(GAAGACNNNNNNN): 231
bsaI(GGTCTCNNNNN): 768
bsaJI(CCNNGG): 5 79 157 373 604 622 716 775 853 1019 1144 1150 1161 1339 1391 1466 1487 1548
bsaWI(WCCGGW): 686
bseRI(GAGGAGNNNNNNNNNN): 1014
bsgI(GTGCAG): 915 1225
bsh1236I(CGCG): 74 80 86 98 152 214 216 398 764 1614 1620
bsiCI(TTCGAA): 20

bsiEI(CGRYCG): 1616

bsiHKAI(GWGCWC): 1361

bslI(CCNNNNNNNGG): 317 368 478 511 680 758 948 1144 1145 1150 1255 1310 1386 1466 1543

bsmAI(GTCTC): 768 1564

bsmAI(GTCTC): 768 1564

bsmBI(CGTCTCNNNNN): 1564

bsmFI(GGGACNNNNNNNNNNNNNN): 828

bsoFI(GCNGC): 106 109 112 115 118 153 166 182 197 200 334 570 788 917 1006 1169 1227 1331 1396 1615 1618

bsp106(ATCGAT): 15

bsp120I(GGGCCC): 838

bsp1286(GDGCHC): 838 985 1022 1109 1278 1361 1482

bspCNI(CTCAGNNNNNNNNN): 464 803 1075 1134 1260

bspDI(ATCGAT): 15

bspEI(TCCGGA): 686

bspMI(ACCTGC): 178 203 454 1105 1216

bspMII(TCCGGA): 686

bsrBI(GAGCGG): 137 1007

bsrDI(GCAATGNN): 277

bsrFI(RCCGGY): 1316

bsrI(ACTGGN): 35 515

bssHII(GCGCGC): 213 215

bssKI(CCNGG): 368 440 604 623 717 854 875 948 1019 1145 1150 1151 1241 1392 1466 1543 1548

bssSI(CTCGTG): 285 1199

bstBI(TTCGAA): 20

bstDSI(CCRYGG): 79 1161 1339 1487

bstEII(GGTNACC): 450

bstF5I(GGATG): 326 662 909 1552

bstNI(CCWGG): 368 440 604 623 717 854 875 948 1019 1241 1392 1466 1548

bstUI(CGCG): 74 80 86 98 152 214 216 398 764 1614 1620
bstYI(RGATCY): 42 53
btgI(CCRYGG): 79 1161 1339 1487
btrI(CACGTC): 540
btsI(GCAGTGNN): 343 698 1088 1283
cac8I(GCNNGC): 162 213 215 330 359 614 645 884 958 1084 1101
cfoI(GCGC): 151 185 213 215 217 635
cfr10I(RCCGGY): 1316
cfrI(YGGCCR): 28 37 154 1616
claI(ATCGAT): 15
csp6I(GTAC): 302 437 800
ddeI(CTNAG): 292 464 803 932 1075 1134 1260 1457
dpnI(GATC): 43 54 242 413 1294
dpnII(GATC): 43 54 242 413 1294
draII(RGGNCCY): 141 837 838
draIII(CACNNNGTG): 1308
drdI(GACNNNNNNGTC): 68 1623
dsaI(CCRYGG): 79 1161 1339 1487
dsaV(CCNGG): 368 440 604 623 717 854 875 948 1019 1145 1150 1151 1241 1392 1466 1543 1548

eaeI(YGGCCR): 28 37 154 1616
eagI(CGGCCG): 1616
earI(CTCTTCNNNN): 459
eciI(GGCGGA): 92
eclXI(CGGCCG): 1616
eco47III(AGCGCT): 634
eco57I(CTGAAG): 581 997
ecoNI(CCTNNNNNAGG): 1255
ecoO109I(RGGNCCY): 141 837 838
ecoRI(GAATTC): 23

ecoRII(CCWGG): 368 440 604 623 717 854 875 948 1019 1241 1392 1466 1548
esp3I(CGTCTC): 1564
fnu4HI(GCNGC): 106 109 112 115 118 153 166 182 197 200 334 570 788 917 1006 1169 1227 1331 1396 1615 1618
fnuDII(CGCG): 74 80 86 98 152 214 216 398 764 1614 1620
fokI(GGATG): 326 662 909 1552
gsuI(CTGGAG): 1017
haeII(RGCGCY): 184 634
haeIII(GGCC): 29 38 143 155 362 371 377 554 617 626 839 1148 1159 1207 1302 1322 1546 1617
hgaI(GACGC): 75 84 96 194 396
hgiAI(GWGCWC): 1361
hhaI(GCGC): 151 185 213 215 217 635
hinPI(GCGC): 151 185 213 215 217 635
hincII(GTYRAC): 393 675 1632
hindII(GTYRAC): 393 675 1632
hinfI(GANTC): 18 288 558 1197 1499 1623 1630
hpaII(CCGG): 40 687 1146 1151 1236 1317 1544
hphI(GGTGA): 264 450 508 526 577 754 899
hpy188III(TCNNGA): 48 190 472 664 686 1626
hpy99I(CGWCG): 122 395
hpyCH4IV(ACGT): 541 673
hpyCH4V(TGCA): 1 255 722 916 1087 1226 1446
ksp632I(CTCTTCNNNN): 459
kspI(CCGCGG): 79
maeI(CTAG): 49 1048 1095 1627
maeII(ACGT): 541 673
maeIII(GTNAC): 451 525 1453
mboI(GATC): 43 54 242 413 1294
mboII(GAAGA): 232 382 460 598

mcrI(CGRYCG): 1616
mluI(ACGCGT): 73 85 97 397
mlyI(GAGTCNNNNN): 288 558 1197 1499 1623 1630
mnlI(CCTC): 5 46 58 64 267 324 373 506 566 619 709 777 836 842 847 872 891 940 992 1016 1059 1074 1133 1255 1324 1335 1348 1376 1472

mroI(TCCGGA): 686
mseI(TTAA): 1067
mslI(CAYNNNNRTG): 350
mspA1I(CMGCKG): 79 113 918 1228
mspI(CCGG): 40 687 1146 1151 1236 1317 1544
mvaI(CCWGG): 368 440 604 623 717 854 875 948 1019 1241 1392 1466 1548
mvnI(CGCG): 74 80 86 98 152 214 216 398 764 1614 1620
mwoI(GCNNNNNNNGC): 30 106 109 112 118 144 153 217 334 363 618 958 987 1079 1160 1182 1547

nciI(CCSGG): 1145 1150 1151 1543
ncoI(CCATGG): 1487
ndeII(GATC): 43 54 242 413 1294
nlaIII(CATG): 131 1114 1366 1488
nlaIV(GGNNCC): 42 141 168 552 689 838 936 1108 1166 1205 1232 1300 1481 1491
notI(GCGGCCGC): 1615
nspBII(CMGCKG): 79 113 918 1228
palI(GGCC): 29 38 143 155 362 371 377 554 617 626 839 1148 1159 1207 1302 1322 1546 1617

pflFI(GACNNNGTC): 1499
pflMI(CCANNNNNTGG): 511
pleI(GAGTCNNNN): 288 558 1197 1499 1623 1630
psiI(TTATAA): 1521
pspAI(CCCGGG): 1150
pspGI(CCWGG): 368 440 604 623 717 854 875 948 1019 1241 1392 1466 1548
pspOMI(GGGCCC): 838

pstI(CTGCAG): 1086 1445
pvuII(CAGCTG): 918
rmaI(CTAG): 49 1048 1095 1627
rsaI(GTAC): 302 437 800
sacII(CCGCGG): 79
salI(GTCGAC): 393 1632
sapI(GCTCTTCNNNN): 458
sau3AI(GATC): 43 54 242 413 1294
sau96I(GGNCC): 142 475 553 689 838 839 1148 1206 1238 1301
scrFI(CCNGG): 368 440 604 623 717 854 875 948 1019 1145 1150 1151 1241 1392 1466
1543 1548

sexAI(ACCWGGT): 439
sfaNI(GCATC): 256 327 723 1539 1553
sfcI(CTRYAG): 272 1086 1445
sfiI(GGCCNNNNNGGCC): 29 362 617
sfuI(TTCGAA): 20
smaI(CCCGGG): 1150
sspI(AATATT): 1439
sstII(CCGCGG): 79
styI(CCWWGG): 157 1487
taiI(ACGT): 541 673
taqI(TCGA): 16 21 60 66 175 394 1633
tfiI(GAWTC): 18
thaI(CGCG): 74 80 86 98 152 214 216 398 764 1614 1620
tru9I(TTAA): 1067
tseI(GCWGC): 112 197 570 917 1227 1331 1396
tsp45I(GTSAC): 451 525
tsp509I(AATT): 24 669
tspRI(NNCAGTGNN): 34 344 425 516 698 1089 1283
tth111I(GACNNNGTC): 1499

xbaI(TCTAGA):	48 1626
xcmI(CCANNNNNNNNNTGG):	349 865
xhoII(RGATCY):	42 53
xmaI(CCCGGG):	1150
xmaIII(CGGCCG):	1616

not found:
aatII(GACGTC),acc65I(GGTACC),aclI(AACGTT),acyI(GRCGYC),aflII(CTTAAG),ageI(ACCGGT),ahaII(GRCGYC),ahaIII(TTTAAA),
ahdI(GACNNNNNGTC),alw44I(GTGCAC),apaLI(GTGCAC),ascI(GGCGCGCC),aseI(ATTAAT),asnI(ATTAAT),asp700(GAANNNNTTC),
asp718(GGTACC),avaIII(ATGCAT),aviII(TGCGCA),avrII(CCTAGG),baeI(NNNNNNNNNNNNNNNACNNNNGTAYCNNNNNNNNNNNN),balI(TGGCCA),
bbrPI(CACGTG),bciVI(GTATCC),bclI(TGATCA),bfrBI(ATGCAT),bfrI(CTTAAG),bglII(AGATCT),blnI(CCTAGG),blpI(GCTNAGC),
bpu1102I(GCTNAGC),bsaAI(YACGTR),bsaBI(GATNNNNATC),bsaHI(GRCGYC),bsaXI(NNNNNNNNNNNNACNNNNNCTCCNNNNNNNNNN),
bsiWI(CGTACG),bsmI(GAATGCN),bsp1407I(TGTACA),bspCI(CGATCG),bspHI(TCATGA),bsrGI(TGTACA),bst1107I(GTATAC),
bst4CI(ACNGT),bstAPI(GCANNNNNTGC),bstXI(CCANNNNNNTGG),bstZ17I(GTATAC),bsu36I(CCTNAGG),celII(GCTNAGC),cpoI(CGGWCCG),
cspI(CGGWCCG),draI(TTTAAA),eam1105I(GACNNNNNGTC),ecl136II(GAGCTC),eco72I(CACGTG),eco81I(CCTNAGG),ecoRV(GATATC),
eheI(GGCGCC),espI(GCTNAGC),fseI(GGCCGGCC),fspI(TGCGCA),hindIII(AAGCTT),hinlI(GRCGYC),hpaI(GTTAAC),hpy188I(TCNGA),
hpyCH4III(ACNGT),kasI(GGCGCC),kpnI(GGTACC),mamI(GATNNNNATC),mfeI(CAATTG),mscI(TGGCCA),mstII(CCTNAGG),munI(CAATTG),
naeI(GCCGGC),narI(GGCGCC),ndeI(CATATG),ngoMI(GCCGGC),nheI(GCTAGC),nruI(TCGCGA),nsiI(ATGCAT),nspHI(RCATGY),
nspI(RCATGY),pacI(TTAATTAA),paeR7I(CTCGAG),pciI(ACATGT),pmeI(GTTTAAAC),pmlI(CACGTG),ppu10I(ATGCAT),ppuMI(RGGWCCY),
pshAI(GACNNNNGTC),psp1406I(AACGTT),pvuI(CGATCG),rcaI(TCATGA),rsrII(CGGWCCG),sacI(GAGCTC),sanDI(GGGWCCC),
sauI(CCTNAGG),sbfI(CCTGCAGG),scaI(AGTACT),sceI(TAGGGATAACAGGGTAAT),sgfI(GCGATCGC),sgrAI(CRCCGGYG),smlI(CTYRAG),
snaBI(TACGTA),snoI(GTGCAC),snoI(GTGCAC),speI(ACTAGT),sphI(GCATGC),splI(CGTACG),srfI(GCCCGGGC),sse8387I(CCTGCAGG),
sstI(GAGCTC),stuI(AGGCCT),swaI(ATTTAAAT),tliI(CTCGAG),vspI(ATTAAT),xhoI(CTCGAG),xmnI(GAANNNNTTC)

This Page is Inserted by IFW Indexing and Scanning Operations and is not part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☑ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.
As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.